What is claimed is:

1. A method of analyzing a subset of nucleic acids within a nucleic acid population, comprising:

(a) providing a population of nucleic acid fragments wherein at least some of said fragments have sequences that are repeated;

(b) denaturing said population of nucleic acid fragments;

(c) incubating said denatured population of nucleic acid fragments under conditions to produce a double-stranded subset of said population of nucleic acids and a single-stranded subset of said population of nucleic acids, wherein under said annealing conditions nucleic acid fragments of said population having repeat sequences preferentially anneal with each other relative to nucleic acid fragments of said population lacking repeat sequences;

(d) separating said single-stranded subset of said population of nucleic acid fragments from said double-stranded subset of said population of nucleic acid fragments;

(e) hybridizing said separated single-stranded subset of said population of nucleic acid fragments to probes on a nucleic acid probe array; and

(f) determining which of said probes on said array hybridize to said single-stranded subset of said population of nucleic acid fragments, thereby analyzing said single-stranded subset of said population of nucleic acid fragments.

2. The method of claim 1, wherein said population of nucleic acid fragments are genomic DNA fragments.

3. The method of claim 2, wherein said genomic DNA fragments are from a human genome.

4. The method of claim 3, wherein said DNA fragments from a human genome are fragments from a same chromosome of different human individuals.

5. The method of claim 1, wherein said separating step is performed by column chromatography.

6. The method of claim 5, wherein said column is a hydroxyapatite column.

7. The method of claim 6, wherein said separating step is performed under conditions whereby said single-stranded subset and said double-stranded are eluted in phosphate buffer.

8. The method of claim 1, wherein said separating step is performed by HPLC.

9. The method of claim 1, wherein said separating step is performed by successively performing hydroxyapatite chromatography and HPLC.

10. The method of claim 1, wherein said probe array comprises a set of probes complementary to a known reference sequence, said reference sequence being substantially identical to a sequence of said population of nucleic acid fragments.

11. The method of claim 10, wherein said population of nucleic acid fragments are from a chromosome from a first individual, and said reference sequences is a corresponding chromosome from a second individual.

12. The method of claim 10, wherein said population of nucleic acid fragments are genomic fragments from a first individual, and said reference sequences are genomic fragments from a second individual of a species closely related to said first individual.

13. The method of claim 10, wherein said population of nucleic acid fragments are genomic fragments from a non-human primate, and said reference sequence is from a human.

14. The method of claim 10, wherein said population of nucleic acid fragments are genomic fragments from a non-human mammal, and said reference sequence is from a human.

15. A method of analyzing a subset of nucleic acids within a nucleic acid population, comprising:

(a) providing a driver population of nucleic acids and a tester population of nucleic acids;

(b) denaturing said driver population of nucleic acids and said tester population of nucleic acids;

(c) annealing said driver population to said tester population to produce a single-stranded subset of nucleic acids and a double-stranded subset of nucleic acids;

(d) immobilizing said driver population of nucleic acids to produce an unimmobilized single-stranded tester subset of nucleic acids, an immobilized double-stranded tester-driver subset of nucleic acids and an immobilized single-stranded driver subset of nucleic acids;

(e) separating said unimmobilized single-stranded tester subset of nucleic acids from said immobilized double-stranded tester-driver subset of nucleic acids and said immobilized single-stranded driver subset of nucleic acids;

(f) hybridizing said unimmobilized single-stranded tester subset of nucleic acids to probes on a nucleic acid probe array; and

(g) determining which of said probes on said array hybridize to said unimmobilized single-stranded tester subset of nucleic acids, thereby analyzing said unimmobilized single-stranded tester subset of nucleic acids.

16. The method of claim 15, wherein said driver population of nucleic acids each bear a tag by which said driver population of nucleic acids can be immobilized to a binding moiety with affinity for said tag.

17. The method of claim 16, wherein said tag is biotin, and said binding moiety is avidin or streptavidin.

18. The method of claim 17, wherein said separating step is performed by immobilizing said immobilized double-stranded tester-driver subset of nucleic acids and said immobilized single-stranded driver subset of nucleic acids via said tags on said driver population.

19. The method of claim 15, wherein said driver population of nucleic acids are genomic DNA from a first source, and said tester population of nucleic acids are genomic DNA from a second source.

20. The method of claim 19, wherein said first source is from a tissue of a first species, and said second source is from a same tissue of a different species.

21. The method of claim 19, wherein said first source is from a first tissue of a first species, and said second source is from a different tissue of said first species.

22. The method of claim 15, wherein said immobilizing step is performed before said annealing step.

23. The method of claim 15, wherein said immobilizing step is performed before said denaturing step.

24. A method of analyzing a subset of nucleic acids within a nucleic acid population, comprising:

(a) providing a driver population of nucleic acids and a tester population of nucleic acids;

(b) denaturing said driver population of nucleic acids and said tester population of nucleic acids;

(c) annealing said driver population to said tester population to produce a single-stranded subset of nucleic acids and a double-stranded subset of nucleic acids;

(d) immobilizing said driver population of nucleic acids to produce an unimmobilized single-stranded tester subset of nucleic acids, an immobilized double-stranded tester-driver subset of nucleic acids and an immobilized single-stranded driver subset of nucleic acids;

(e) separating said unimmobilized single-stranded tester subset of nucleic acids from said immobilized double-stranded tester-driver subset of nucleic acids and said immobilized single-stranded driver subset of nucleic acids;

(f) dissociating said immobilized double-stranded tester-driver subset of nucleic acids to produce a subset of complementary tester nucleic acids and a subset of immobilized complementary driver nucleic acids;

(g) separating said subset of complementary tester nucleic acids from said subset of immobilized complementary driver nucleic acids;

(h) hybridizing said subset of complementary tester nucleic acids to probes on a nucleic acid probe array;

(i) determining which of said probes on said array hybridize to said subset of complementary tester nucleic acids, thereby analyzing said subset of complementary tester nucleic acids.

25. The method of claim 24, wherein said driver population is a population of genomic DNA fragments, and said tester population is mRNA or nucleic acids derived therefrom.

26. The method of claim 24, wherein said driver population is a population of genomic DNA fragments from a first source, and said tester population is genomic DNA from a second source.

27. The method of claim 26, wherein said tester population is from a genome of a first individual, and said driver population is from a genome of a different individual of a same species as said first individual.

28. The method of claim 26, wherein said tester population is from a genome of a first individual, and said driver population is from a genome of an individual of a different species than said first individual.

29. The method of claim 24, wherein either said driver population or said tester population or both said driver and said tester populations is a PCR amplification product.

30. The method of claim 24, wherein said driver population is from a plurality of noncontiguous regions of a genome of a species.

31. The method of claim 30, wherein said driver population is from at least ten noncontiguous regions.

32. The method of claim 24, wherein said driver population is mRNA or nucleic acids derived therefrom, and said tester population is genomic DNA.

33. The method of claim 24, wherein said driver population is mRNA or nucleic acids derived therefrom from a first source, and said tester population is mRNA or nucleic acids derived therefrom from a second source.

34. The method of claim 33, wherein said first source is from a tissue of a first species, and said second source is from a same tissue of a different species.

35. The method of claim 33, wherein said first source is from a first tissue of a first species, and said second source is from a different tissue of said first species.

36. The method of claim 24, wherein said immobilizing step is performed before said annealing step.

37. The method of claim 24, wherein said immobilizing step is performed before said first denaturing step.

38. The method of claim 24, wherein said driver population of nucleic acids each bear a tag by which said driver population can be immobilized to a binding moiety with affinity for said tag.

39. The method of claim 38, wherein said tag is biotin, and said binding moiety is avidin or streptavidin.

40. The method of claim 39, wherein said first separating step is performed by immobilizing said driver population of nucleic acids and tester population of nucleic acids hybridized to said driver population via said tags on said driver population.